



SEQUENCE LISTING

<110> MacPhee, Colin Houston
Tew, David Graham
Southan, Christopher Donald
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Gloger, Israel Simon
Lawrence, Geoffrey Mark Prouse
Rice, Simon Quentyn John

<120> Lipoprotein Associated Phospholipase A2,
Inhibitors Thereof and Use of the Same in Diagnosis and
Therapy

<130> P30693C4X1C1

<140> 09/922,067
<141> 2001-08-03

<150> 09/193,130
<151> 2000-11-28

<150> 08/387,858
<151> 1994-06-24

<150> PCT/GB94/01374
<151> 1994-06-24

<150> GB 9313144.9
<151> 1993-06-25

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 37
<212> PRT
<213> Homo sapien

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1 5 10 15
Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His
20 25 30
Lys Asp Phe Asp Gln
35

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<211> 30

<212> PRT

<213> Homo sapien

<400> 2

Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro
1 5 10 15
Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn
20 25 30

<210> 3

<211> 27

<212> PRT

<213> Homo sapien

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Gln Tyr Ile Asn Pro Ala Val Met Ile Thr Ile Arg Gly Ser Val His
1 5 10 15
Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly
20 25

<210> 4

<211> 19

<212> PRT

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Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr
1 5 10 15
Pro Ala Asn

<210> 5

<211> 420

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> 265, 390, 395, 403, 406

<223> n = A,T,C or G

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aaaaaaccta ttttaatcct aattgtattt ctctattcct gaagagttct gtaacatgat 60
gtgttgattg gttgtgttaa tgttggtccc tggaataaga ttctcatcat ctctttcaat 120
caagcagtc cactgatcaa aatctttatg aagtcctaaa tgcttttgta agaatgctaa 180
tgaagctttg ttgctaagat caatagctgc atttgaatct atgtctccct ttaatttgag 240
catgtgtcca attattttgc cagtn gcaaaa agtgaagtca gcaaaattct ggtggactga 300
acccctgatt gtaatcatct ttctttcttt atcaggtgag tagcattttt tcatTTTTat 360
gatattagca ggatattgga aatattcagn gttgntaaaa agngggnggct gagggattct 420

<210> 6

<211> 379

<212> DNA

<213> Unknown

<220> Homo sapien

<221> misc_feature

<222> 84

<223> n = A,T,C or G

<400> 6

tgctaataatc ataaaaatga aaaaatgcta ctcacctgat aaagaagaa agatgattac 60

aatcaggggt tcagtcacc aganttttgc tgacttcaact ttgcaactg gcaaaataat 120
tggacacatg ctcaaattaa agggagacat agattcaaat gtagctattg atcttagcaa 180
caaagcttca ttgacattct taaaaagca tttaggactt cataaagatt ttgttcagtg 240
ggactgcttg attgaaggag atgatgagaa tcttattcca gggaccaaca ttaacacaac 300
caattcaaca catcatgttt acagaacttc ttccaggaa taggaggaaa tacaattggg 360
gtttaaaata ggtttttttt 379

<210> 7

<211> 279

<212> DNA

<213> Unknown

<220> Homo sapien

<221> misc_feature

<222> 257

<223> n = A,T,C or G

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gaagaatgca ttgattttaa agtttgatat ggaacaactg aaggactcta ttgataggga 60
aaaaatagca gtaattggac attcttttgg tggagcaacg gttattcaga ctcttagtga 120
agatcagaga ttcagatgtg gtattgccct ggatgcatgg atgtttccac tgggtgatga 180
agtatatccc agaattccct agccctcttt tttatcaac tctgaatatt tccaatatcc 240
tgctaataatc ataaaantgg aaaaatgcta ctcacctgg 279

<210> 8

<211> 572

<212> DNA

<213> Homo sapien

<400> 8

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gatcagagat tcagatgtgg tattgccctg gatgcatgga tgtttccact ggggtgatga 120
gtatatccca gaattcccca gccctctttt ttatcaact ctgaatatct ccaatatcct 180
gctaatatca taaaaatgaa aaaaatgtac tcacctgata aagaaagaaa gatgattaca 240
atcagggggt cagtcaccca gaattttgct gacttcaact ttgcaactgg caaaataatt 300
ggacacatgc tcaaattaaa gggagacata gattcaaatg tagctattga tcttagcaac 360
aaagcttcat cagcattctt acaaaagcat ttaggacttc ataaagattt tgatcagtgg 420
gactgcttga ttgaaggaga tgatgagaat cttattccag ggaccaacat taacacaacc 480
aatcaacaca tcattgttaca gaactcttca ggaatagaga aatacaatta ggattaaaat 540
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1 5

cat gtg ctt ttc tgc ctc tgc ggc tgc ctg gct gtg gtt tat cct ttt 103
His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe
10 15 20

gac tgg caa tac ata aat cct gtt gcc cat atg aaa tca tca gca tgg 151
Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp
25 30 35

gtc aac aaa ata caa gta ctg atg gct gct gca agc ttt ggc caa act 199
Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr
40 45 50

aaa atc ccc cgg gga aat ggg cct tat tcc gtt ggt tgt aca gac tta 247
Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu
55 60 65 70

atg ttt gat cac act aat aag ggc acc ttc ttg cgt tta tat tat cca 295
Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro
75 80 85

tcc caa gat aat gat cgc ctt gac acc ctt tgg atc cca aat aaa gaa 343
Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu
90 95 100

tat ttt tgg ggt ctt agc aaa ttt ctt gga aca cac tgg ctt atg ggc 391

Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly Thr His Trp Leu Met Gly	
105	110 115
aac att ttg agg tta ctc ttt ggt tca atg aca act cct gca aac tgg	439
Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr Pro Ala Asn Trp	
120	125 130
aat tcc cct ctg agg cct ggt gaa aaa tat cca ctt gtt gtt ttt tct	487
Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr Pro Leu Val Val Phe Ser	
135	140 145 150
cat ggt ctt ggg gca ttc agg aca ctt tat tct gct att ggc att gac	535
His Gly Leu Gly Ala Phe Arg Thr Leu Tyr Ser Ala Ile Gly Ile Asp	
155	160 165
ctg gca tct cat ggg ttt ata gtt gct gct gta gaa cac aga gat aga	583
Leu Ala Ser His Gly Phe Ile Val Ala Ala Val Glu His Arg Asp Arg	
170	175 180
tct gca tct gca act tac tat ttc aag gac caa tct gct gca gaa ata	631
Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp Gln Ser Ala Ala Glu Ile	
185	190 195
ggg gac aag tct tgg ctc tac ctt aga acc ctg aaa caa gag gag gag	679
Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr Leu Lys Gln Glu Glu Glu	
200	205 210
aca cat ata cga aat gag cag gta cgg caa aga gca aaa gaa tgt tcc	727
Thr His Ile Arg Asn Glu Gln Val Arg Gln Arg Ala Lys Glu Cys Ser	
215	220 225 230
caa gct ctc agt ctg att ctt gac att gat cat gga aag cca gtg aag	775
Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp His Gly Lys Pro Val Lys	
235	240 245
aat gca tta gat tta aag ttt gat atg gaa caa ctg aag gac tct att	823
Asn Ala Leu Asp Leu Lys Phe Asp Met Glu Gln Leu Lys Asp Ser Ile	
250	255 260
gat agg gaa aaa ata gca gta att gga cat tct ttt ggt gga gca acg	871

Asp Arg Glu Lys Ile Ala Val Ile Gly His Ser Phe Gly Gly Ala Thr	
265	270 275
gtt att cag act ctt agt gaa gat cag aga ttc aga tgt ggt att gcc	919
Val Ile Gln Thr Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Ile Ala	
280	285 290
ctg gat gca tgg atg ttt cca ctg ggt gat gaa gta tat tcc aga att	967
Leu Asp Ala Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile	
295	300 305 310
cct cag ccc ctc ttt ttt atc aac tct gaa tat ttc caa tat cct gct	1015
Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala	
315	320 325
aat atc ata aaa atg aaa aaa tgc tac tca cct gat aaa gaa aga aag	1063
Asn Ile Ile Lys Met Lys Lys Cys Tyr Ser Pro Asp Lys Glu Arg Lys	
330	335 340
atg att aca atc agg ggt tca gtc cac cag aat ttt gct gac ttc act	1111
Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr	
345	350 355
ttt gca act ggc aaa ata att gga cac atg ctc aaa tta aag gga gac	1159
Phe Ala Thr Gly Lys Ile Ile Gly His Met Leu Lys Leu Lys Gly Asp	
360	365 370
ata gat tca aat gca gct att gat ctt agc aac aaa gct tca tta gca	1207
Ile Asp Ser Asn Ala Ala Ile Asp Leu Ser Asn Lys Ala Ser Leu Ala	
375	380 385 390
ttc tta caa aag cat tta gga ctt cat aaa gat ttt gat cag tgg gac	1255
Phe Leu Gln Lys His Leu Gly Leu His Lys Asp Phe Asp Gln Trp Asp	
395	400 405
tgc ttg att gaa gga gat gat gag aat ctt att cca ggg acc aac att	1303
Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu Ile Pro Gly Thr Asn Ile	
410	415 420
aac aca acc aat caa cac atc atg tta cag aac tct tca gga ata gag	1351

Asn Thr Thr Asn Gln His Ile Met Leu Gln Asn Ser Ser Gly Ile Glu
425 430 435

aaa tac aat t 1361
Lys Tyr Asn
440

<210> 10
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<212> PRT
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<400> 10
Gln Tyr Ile Asn Pro Val Ala
1 5

<210> 11
<211> 20
<212> PRT
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<400> 11
Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr
1 5 10 15
Phe Ala Thr Gly
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<210> 12
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<212> PRT
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<400> 12
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1 5

<210> 13

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<212> PRT

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<400> 13

Gln Tyr Ile Asn Pro

1

5